

Introduction to Single-cell RNA-seq analysis

Harvard Chan Bioinformatics Core



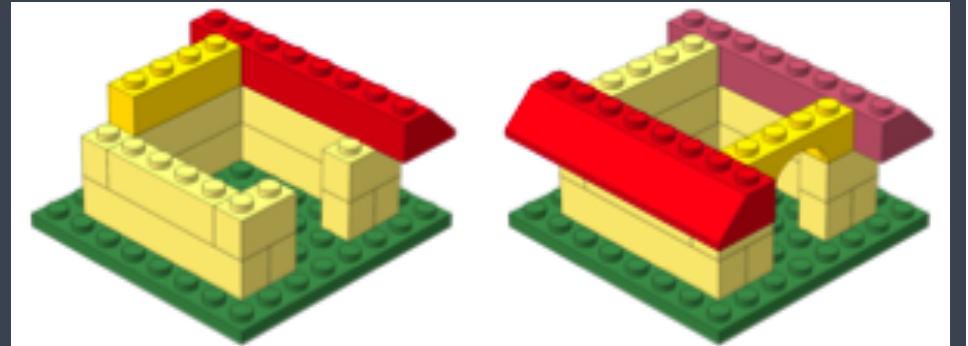
<https://tinyurl.com/hbc-scrnaseq-online>

Learning Objectives



- ✓ Describe best practices for designing a Single-cell RNA-seq experiment
- ✓ Describe steps in a Single-cell RNA-seq analysis workflow.
- ✓ Use Seurat and associated tools to perform analysis of single-cell expression data, including data filtering, QC, clustering, and marker identification

Survey



<https://tinyurl.com/scRNAseq-online>

Useful Resources

Computational packages for single-cell analysis:

<http://bioconductor.org/packages/devel/workflows/html/simpleSingleCell.html>

<https://satijalab.org/seurat/>

<https://scanpy.readthedocs.io/>

<https://github.com/seandavi/awesome-single-cell>

Online courses:

<https://hemberg-lab.github.io/scRNA.seq.course/>

<https://github.com/SingleCellTranscriptomics>

Resources for scRNA-seq Sample Prep:

<https://www.protocols.io/>

<https://support.10xgenomics.com/single-cell-gene-expression/sample-prep>

<https://community.10xgenomics.com/>

Thanks!

- Luciano Martelotto, HMS
- Victor B. Barrera, HBC

Contact us!

Training team ✉ : hbctraining@hsph.harvard.edu

Consulting ✉ : bioinformatics@hsph.harvard.edu

 [@bioinfocore](https://twitter.com/bioinfocore)

These materials have been developed by members of the teaching team at the Harvard Chan Bioinformatics Core (HBC). These are open access materials distributed under the terms of the Creative Commons Attribution license (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

